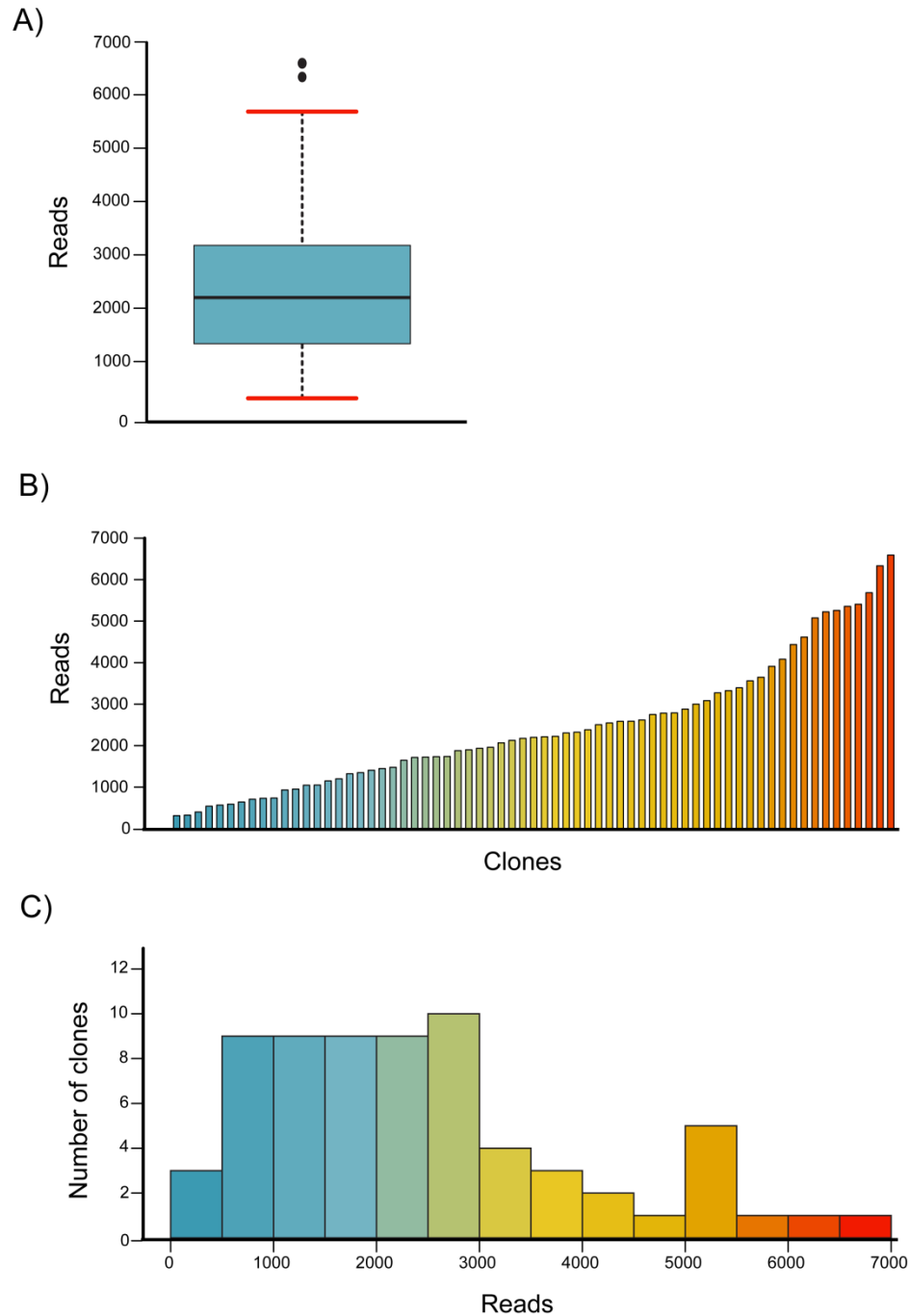


**Figure S1: Validation of *Evx1* screening primers.** The desired ~200bp *Evx1* amplicon can be observed in the wildtype clone (lane 2). CRISPR-Cas9 induced deletions can be observed in other clones by a reduction in PCR product size.



**Figure S2: Coverage statistics for CRISPR-Cas9 screening sequencing. A)** Box and whisker plot demonstrating the relatively even sequencing coverage of each clone. The majority of clones have coverage between ~1200 and ~3100 fold. **B)** Sequencing coverage for each individual clone. **C)** Histogram of sequencing coverage for each clone.